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BOOK REVIEW

Advances in Cladistics: Proceedings of the First Meeting of the Willi Hennig Society.—V. A. Funk and D. R. Brooks (eds.). 1981. New York Botanical Garden, New York. 250 pp. $29.50.

The Proceedings of the First Meeting of the Willi Hennig Society are appropriately titled *Advances in Cladistics.* Much of the debate concerning cladistics over the last few years has comprised repetition of arguments (e.g., Mayr, 1981), many of which have been repeatedly refuted. As J. S. Farris indicates in the Founder's Address, the Hennig Society will serve as a forum for advancing phylogenetic systematics as a science, by providing an opportunity for diverse workers to debate within a cladistic framework. The 13 papers contained herein form an interesting cross-section of current research in theory and application, and show that there are many areas for further development. The meetings from which these papers were drawn (which occurred in October of 1980) have been reviewed by Schuh (1981).

The papers are grouped in four sections. In the first, "Cladistics and Molecular Biology", Farris provides a landmark paper on the use of distance data in phylogenetic analysis. He discusses techniques for analyzing immunological distances, then examines various other types of biochemical distances, and concludes with a general treatment of distance measures. He first devotes considerable space to refutation of the contention of Prager and Wilson (1978) for general superiority of the Fitch-Margoliash method to the Distance Wagner procedure of Farris. After showing their comparisons to be improper he alters his algorithm to fit branch lengths so as to allow better fit in terms of percent standard deviation (i.e., negative branch lengths). This leads to discussion of the bases for measuring fit, and from that he proceeds to consider the effect of nonmetricity on distance measures. As he demonstrates, this vitiates the interpretation of such measures as amounts of evolutionary change between taxa, to the extent of rendering them useless for constructing evolutionary trees. Therefore the concept of a molecular clock as drawn from studies using immunological and Nei's distances is unsupported (since a measure must be ultrametric to show clocklike behavior). He then shows that Euclidean metrics are not interpretable as change either, and that whereas the Manhattan metric is, it can be misleading in terms of treatment of homoplasious characters. Further, sequence differences and the Manhattan metric applied to frequency data are shown to lead to uninterpretable branch lengths. From these conclusions he is led to recommend analyzing character data directly rather than via distance techniques.

Farris' paper has already had a pronounced effect on approaches to genetic distance data. For example, J. Felsenstein at the Evolution meetings in June of 1982 suggested changing the interpretation of the distances from actual phenetic distance to expected (in the statistical sense) distance, and thus permitting branch length fitting. This is in line with Felsenstein's inveterate approach to phylogenetic analysis as a statistical problem, but even if his interpretation is adopted, any molecular clock still needs repair.

D. L. Swofford's paper describes a modification of Farris' Distance Wagner procedure to incorporate all three addition criteria described by Farris in 1972 simultaneously. He then outlines a method for optimizing Distance branch lengths after the initial construction of the tree which allows proper comparison in terms of the "F" statistic of Prager and Wilson (1978). His procedure is quite different from Farris' in the foregoing paper, but his results in re Prager and Wilson are the same. Their logic was flawed and their comparisons when properly done show general superiority for Distance Wagner. Swofford amplifies on certain points made by Farris, and concludes that a defined algorithm such as Distance Wagner is generally more efficient than trial-and-error methods. He rationalizes the use of distance data on the pragmatic grounds that biochemical systematists will undoubtedly continue to rely on distance measures, which is no doubt true. However, in view of the enormous sums expended on such studies they ought to be encouraged to concoct some better justification. Swofford and Selander (1981) describe a Fortran program that will perform his modified procedure.

M. F. Mickevich and C. Mitter, in the third and final paper in this section, compare methods for coding characters of terminal taxa when the characters vary within taxa. Together with Mickevich's paper on quantitative biogeography, this represents the first published exposition of Mickevich's "transformation series analysis" (the term is somewhat sententiously capitalized everywhere in the book except the index). The method is a further formalization for assigning polarities to multistate characters so as to obtain best fit to a given cladogram, ordering states without requiring a pre-defined polarity. In the application to coding the authors first outline the three optimality criteria they use: consistency (degree of fit between classification-implied and data character distributions), boldness (ability to specify a hierarchy) and "Occam's Probative" (which might be characterized as constraining results to the possible) and then compare three coding methods using electromorph data. These are 1) "Independent alleles", where the alleles are the characters and any one can evolve into any other at the same locus. They consider treating combinations of these as quantitative characters, or as binary characters. 2) "Shared alleles", in which the locus is the character and the allelic combinations its states. When more than two alleles occur they are ordered such that states are linked to those with which they share the most alleles. 3) The locus is the character and allelic combinations the states, with order inferred by transformation series analysis. Using a variety of data sets, they show a better performance for the third coding method. They conclude by emphasizing the applicability of this method to other sorts of polymorphic characters, and in an intriguing idea, suggest comparing this method with other types of coding methods developed on the basis of evolutionary assumptions about particular characters as tests of those assumptions.

The second section, "Theoretical Cladistics", is monobasic, comprising D. R. Brooks' paper on treating classifications as languages. He suggests various criteria for best classification from an application of an entropy concept. This approach is here more successful than in Wiley and Brooks (1982). The criteria converge on parsimony, and he concludes by analogizing his approach with those of Nelson (1979) and Farris (1969). His treatment is more general than that of Farris (1979), in that he considers aspects of the information within the terminal taxa, whereas Farris treated this as a constant and analyzed transmission of this information, but it is less applicable in that his criteria could be argued (I suppose) and there is ambiguity in the relationship of the measures for minimum entropy he compares (e.g., his treatment of Nelson's "term information").

The next section, "Botanical Cladistics", includes five papers. Three of these (Sanders, Bolick and Churchill) are cladistic analyses of various plant groups, and are presumably included in this volume in order to demonstrate that, yes, phylogenetic systematics can be done with plants. However, at least the synopsis provided by Churchill (complete with the Latin diagnoses of new taxa) seems quite out of place. There are scattered fallacies throughout some of these papers: Sanders lists four assumptions of Hennigian cladistics, none of which are necessary; he and Funk frequently use "outgroup" for "sister-group"; Churchill speaks of methods that employ the axioms of evolution; Sanders terms bushes resolved; Funk states that a cladistic analysis involving non-monophyletic groups is futile; synapomorphy and autapomorphy are frequently confused; etc. These statements, recalling as they do the misunderstandings prevalent in *Systematic Zoology* debates of ten years ago, indicate that botanists are not very advanced in their understanding of the methods. Although there has of late been considerable print expended on the issue of whether cladistics has somehow been transformed from Hennig's methods, the transformation has been in perception. The methods are just that, a variety of analytical procedures that may be applied to a given data set. Whether or not that data set is evolutionarily clean is irrelevant. Further, the general tenor to the arguments in favor of applying cladistic methods, implying that zoological studies are easy by comparison, is occasionally aggravating.

Withal, certain aspects of these papers are instructive. Funk has an extended discussion of the treatment of putative hybrids in an analysis, concluding, as does Wagner (1980), that they should be removed prior to the construction of the cladogram, to which they can be added like so many ornaments afterwards. This problem is more thoroughly examined here than in theoretical treatments by zoologists. Bremer and Wanntorp give an interesting comparison of cladistic and traditional classifications of major groups of organisms, arguing for progress in classification.

The final section, "Biogeography and Cladistics", contains 4 papers. In the first, Brooks, T. B. Thorson and M. A. Mayes present a study of freshwater stingray biogeography, testing four narrative hypotheses, each encompassing several points, such as the monophyly and origin of the group, on the basis of assertions about the parasite fauna of these fish. They construct cladograms for helminth parasites, show Pacific relationships and are able to define areas of endemism that correspond to those shown by other fishes. They further suggest that an outgroup genus of stingrays may be paraphyletic because of the pattern of interrelationships shown by the parasites. However, only two of the parasite groups force this interpretation (figs. 6 and 11). All in all, an excellent example of the "coevolutionary" approach.

C. J. Humphries also presents an interesting study, on the celebrated *Nothofagus*. Constructing a cladogram of the species and then a reduced area cladogram, he compares this with four geological cladograms and is able to show only a Laurasia/Gondwanaland pattern. Comparison with reduced area cladograms of a variety of other organisms shows considerable incongruence. Thus *Nothofagus* is relatively uninformative about interrelationships of the southern land masses. Throughout his paper there is a very good emphasis that acceptance of continental drift only provides a plausible dispersal route for a non-analytic biogeography.

Mickevich contributes an important paper on quantitative biogeography. In it she shows how transformation series analysis (which is explained by examples and figures that allow one to perform the procedure) can be of great use in biogeography. The method can extract the general pattern (a "biogeographic map") from a set of area cladograms. It is a logical extension of parsimony algorithms to analytic biogeography, which may thus be automated. Readers attempting to follow her example drawn from Rosen (1978) should note that there are several typos and there are missing values for row "D" in Table II: the 4 should be a 2. Also her exclusion of area 7 on the *Heterandria* cladogram (fig. 7a) from the transformation into area states may be an oversight, but points out some ambiguity in this part of the process (cf. her assignments of area states with figs. 1 and 2 in Platnick's paper).

Platnick has the final say in a paper explicating the thoughts of Nelson and Platnick (1981) on dealing with widespread taxa in biogeography. He too uses the example from Rosen (1978), analyzing the cladograms under two different assumptions about the history of the groups. It is interesting that Mickevich's method, when area states are defined as she does and area 7 omitted, gives the same pattern under both assumptions. This again shows ambiguity in the assignment of area states. If the localities are used as area states (only areas 2 and 10 overlap), the problem of combinability discussed by Platnick remains. Whether the greater informativeness under Platnick's second assumption (amounting here to disjunction, then fusion of areas) is more than *ad hoc* can at least be tested as he suggests.

In summary, as published symposia go, the quality of papers in this book is quite good. In these days of offset printing of this type of publication, it is refreshing to see superb quality paper and excellent binding for a paperback. However, the rather exorbitant price ($29.50) illustrates why offset printing is used so widely for symposia. Considering that there are no entomological papers in the book, readers of this journal interested in these proceedings are likely to be systematists interested in some of the theoretical papers. That being the case, they would probably be better off photocopying about three or four papers and the unified bibliography than purchasing the whole volume.—*James M. Carpenter, Department of Entomology, Cornell University, Ithaca, New York 14853.*

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